



PCT10

RAW SEQUENCE LISTING

DATE: 04/14/2003

PATENT APPLICATION: US/10/088,639A

TIME: 09:46:49

Input Set : N:\CrF4\04032003\J088639.raw

Output Set: N:\CRF4\04142003\J088639A.raw

1 <110> APPLICANT: Brodin, Thomas
 2 Karlstrom, Pia J.
 3 Ohlsson, Lennart G.
 4 Tordsson, Jesper M.
 5 Kearney, Philip P.
 6 Nilson, Bo H.K.
 7 <120> TITLE OF INVENTION: Novel Compounds
 8 <130> FILE REFERENCE: 003300-920
 9 <140> CURRENT APPLICATION NUMBER: US/10/088,639A
 C--> 10 <141> CURRENT FILING DATE: 1999-10-28
 11 <150> PRIOR APPLICATION NUMBER: SE 9903895-2
 12 <151> PRIOR FILING DATE: 1999-10-28
 13 <160> NUMBER OF SEQ ID NOS: 51
 14 <170> SOFTWARE: PatentIn Ver. 2.1
 16 <210> SEQ ID NO: 1
 17 <211> LENGTH: 747
 18 <212> TYPE: DNA
 19 <213> ORGANISM: Macaca fascicularis
 20 <220> FEATURE:
 21 <221> NAME/KEY: CDS
 22 <222> LOCATION: (1)..(747)
 23 <223> OTHER INFORMATION: Coding sequence VL (1-109) - modified Huston
 24 linker (110-127) - VH (128-249)
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 28 1 5 10 15
 29 aca gtc agg atg acc tgc caa gga gac agc ctc aaa acc tat tat gca 96
 30 Thr Val Arg Met Thr Cys Gln Gly Asp Ser Leu Lys Thr Tyr Tyr Ala
 31 20 25 30
 32 agc tgg tac cag cag aag cca ggc cag gtc cct gtg ctg gtc atc tat 144
 33 Ser Trp Tyr Gln Gln Lys Pro Gly Gln Val Pro Val Leu Val Ile Tyr
 34 35 40 45
 35 ggt aac aac tac cgg ccc tca ggg atc cca ggc cga ttc tct ggc tcc 192
 36 Gly Asn Asn Tyr Arg Pro Ser Gly Ile Pro Gly Arg Phe Ser Gly Ser
 37 50 55 60
 38 tgg tca gga aac aca gct tcc ttg acc atc act gcg gct cag gtg gaa 240
 39 Trp Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Ala Ala Gln Val Glu
 40 65 70 75 80
 41 gat gag gct gac tat tac tgt aac tcc tgg gac agc agc ggt acc cat 288
 42 Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Trp Asp Ser Ser Gly Thr His
 43 85 90 95
 44 ccg gta ttc ggc gga ggg acc cgg gtg acc gtc cta ggt caa gcc aac 336

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45      Pro Val Phe Gly Gly Gly Thr Arg Val Thr Val Leu Gly Gln Ala Asn
46                100                105                110
47      ggt gaa ggc ggc tct ggt ggc ggg gga tcc gga ggc ggc ggt tct gag   384
48      Gly Glu Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu
49                115                120                125
50      gtg cag ttg gtg gag tct ggg gga ggc ttg gta aag cct ggg ggg tcc   432
51      Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly Ser
52                130                135                140
53      ctg aga ctc tct tgt gta gcc tct ggg tcc atc ttc agt agc tct gtt   480
54      Leu Arg Leu Ser Cys Val Ala Ser Gly Ser Ile Phe Ser Ser Ser Val
55      145                150                155                160
56      atg cac tgg gtc cgc cag gct cca gga aag ggt ctg gag tgg gtc tca   528
57      Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
58                165                170                175
59      gtt att agt gaa aat ggg cgt acc att aac tac gca gac tct gtg aag   576
60      Val Ile Ser Glu Asn Gly Arg Thr Ile Asn Tyr Ala Asp Ser Val Lys
61                180                185                190
62      ggc cga ttc acc atc tcc aga gac aac gcc aag aac tca ctg ttt ctg   624
63      Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Phe Leu
64      195                200                205
65      cag atg aac agc ctg aca ggc gag gac acg gcc gtc tat tac tgt agt   672
66      Gln Met Asn Ser Leu Thr Gly Glu Asp Thr Ala Val Tyr Tyr Cys Ser
67      210                215                220
68      aga gag ggg gga cct gga aca acg tcc aac cgg ctc gat gcc tgg ggc   720
69      Arg Glu Gly Gly Pro Gly Thr Thr Ser Asn Arg Leu Asp Ala Trp Gly
70      225                230                235                240
71      ccg gga gtc ctg gtc acc gtt tcc tca                               747
72      Pro Gly Val Leu Val Thr Val Ser Ser
73                245
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76 <211> LENGTH: 249
77 <212> TYPE: PRT
78 <213> ORGANISM: Macaca fascicularis
79 <220> FEATURE:
80 <223> OTHER INFORMATION: Coding sequence VL (1-109) - modified Huston
81 linker (110-127) - VH (128-249)
82 <400> SEQUENCE: 2
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84      1                5                10                15
85      Thr Val Arg Met Thr Cys Gln Gly Asp Ser Leu Lys Thr Tyr Tyr Ala
86      20                25                30
87      Ser Trp Tyr Gln Gln Lys Pro Gly Gln Val Pro Val Leu Val Ile Tyr
88      35                40                45
89      Gly Asn Asn Tyr Arg Pro Ser Gly Ile Pro Gly Arg Phe Ser Gly Ser
90      50                55                60
91      Trp Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Ala Ala Gln Val Glu
92      65                70                75                80
93      Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Trp Asp Ser Ser Gly Thr His
94      85                90                95

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95      Pro Val Phe Gly Gly Gly Thr Arg Val Thr Val Leu Gly Gln Ala Asn
96                100                105                110
97      Gly Glu Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu
98                115                120                125
99      Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly Ser
100      130                135                140
101      Leu Arg Leu Ser Cys Val Ala Ser Gly Ser Ile Phe Ser Ser Ser Val
102      145                150                155                160
103      Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
104      165                170                175
105      Val Ile Ser Glu Asn Gly Arg Thr Ile Asn Tyr Ala Asp Ser Val Lys
106      180                185                190
107      Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Phe Leu
108      195                200                205
109      Gln Met Asn Ser Leu Thr Gly Glu Asp Thr Ala Val Tyr Tyr Cys Ser
110      210                215                220
111      Arg Glu Gly Gly Pro Gly Thr Thr Ser Asn Arg Leu Asp Ala Trp Gly
112      225                230                235                240
113      Pro Gly Val Leu Val Thr Val Ser Ser
114      245
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117 <211> LENGTH: 1073
118 <212> TYPE: PRT
119 <213> ORGANISM: Human
120 <220> FEATURE:
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125      Leu Ser Arg Leu Gly Ala Ala Phe Asn Leu Asp Thr Arg Glu Asp Asn
126      20          25          30
127      Val Ile Arg Lys Tyr Gly Asp Pro Gly Ser Leu Phe Gly Phe Ser Leu
128      35          40          45
129      Ala Met His Trp Gln Leu Gln Pro Glu Asp Lys Arg Leu Leu Leu Val
130      50          55          60
131      Gly Ala Pro Arg Gly Glu Ala Leu Pro Leu Gln Arg Ala Asn Arg Thr
132      65          70          75          80
133      Gly Gly Leu Tyr Ser Cys Asp Ile Thr Ala Arg Gly Pro Cys Thr Arg
134      85          90          95
135      Ile Glu Phe Asp Asn Asp Ala Asp Pro Thr Ser Glu Ser Lys Glu Asp
136      100         105         110
137      Gln Trp Met Gly Val Thr Val Gln Ser Gln Gly Pro Gly Gly Lys Val
138      115         120         125
139      Val Thr Cys Ala His Arg Tyr Glu Lys Arg Gln His Val Asn Thr Lys
140      130         135         140
141      Gln Glu Ser Arg Asp Ile Phe Gly Arg Cys Tyr Val Leu Ser Gln Asn
142      145         150         155         160
143      Leu Arg Ile Glu Asp Asp Met Asp Gly Gly Asp Trp Ser Phe Cys Asp
144      165         170         175

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145   Gly Arg Leu Arg Gly His Glu Lys Phe Gly Ser Cys Gln Gln Gly Val
146               180                      185                      190
147   Ala Ala Thr Phe Thr Lys Asp Phe His Tyr Ile Val Phe Gly Ala Pro
148               195                      200                      205
149   Gly Thr Tyr Asn Trp Lys Gly Ile Val Arg Val Glu Gln Lys Asn Asn
150               210                      215                      220
151   Thr Phe Phe Asp Met Asn Ile Phe Glu Asp Gly Pro Tyr Glu Val Gly
152   225                      230                      235                      240
153   Gly Glu Thr Glu His Asp Glu Ser Leu Val Pro Val Pro Ala Asn Ser
154               245                      250                      255
155   Tyr Leu Gly Phe Ser Leu Asp Ser Gly Lys Gly Ile Val Ser Lys Asp
156               260                      265                      270
157   Glu Ile Thr Phe Val Ser Gly Ala Pro Arg Ala Asn His Ser Gly Ala
158               275                      280                      285
159   Val Val Leu Leu Lys Arg Asp Met Lys Ser Ala His Leu Leu Pro Glu
160               290                      295                      300
161   His Ile Phe Asp Gly Glu Gly Leu Ala Ser Ser Phe Gly Tyr Asp Val
162   305                      310                      315                      320
163   Ala Val Val Asp Leu Asn Lys Asp Gly Trp Gln Asp Ile Val Ile Gly
164               325                      330                      335
165   Ala Pro Gln Tyr Phe Asp Arg Asp Gly Glu Val Gly Gly Ala Val Tyr
166               340                      345                      350
167   Val Tyr Met Asn Gln Gln Gly Arg Trp Asn Asn Val Lys Pro Ile Arg
168               355                      360                      365
169   Leu Asn Gly Thr Lys Asp Ser Met Phe Gly Ile Ala Val Lys Asn Ile
170               370                      375                      380
171   Gly Asp Ile Asn Gln Asp Gly Tyr Pro Asp Ile Ala Val Gly Ala Pro
172   385                      390                      395                      400
173   Tyr Asp Asp Leu Gly Lys Val Phe Ile Tyr His Gly Ser Ala Asn Gly
174               405                      410                      415
175   Ile Asn Thr Lys Pro Thr Gln Val Leu Lys Gly Ile Ser Pro Tyr Phe
176               420                      425                      430
177   Gly Tyr Ser Ile Ala Gly Asn Met Asp Leu Asp Arg Asn Ser Tyr Pro
178               435                      440                      445
179   Asp Val Ala Val Gly Ser Leu Ser Asp Ser Val Thr Ile Phe Arg Ser
180               450                      455                      460
181   Arg Pro Val Ile Asn Ile Gln Lys Thr Ile Thr Val Thr Pro Asn Arg
182   465                      470                      475                      480
183   Ile Asp Leu Arg Gln Lys Thr Ala Cys Gly Ala Pro Ser Gly Ile Cys
184               485                      490                      495
185   Leu Gln Val Lys Ser Cys Phe Glu Tyr Thr Ala Asn Pro Ala Gly Tyr
186               500                      505                      510
187   Asn Pro Ser Ile Ser Ile Val Gly Thr Leu Glu Ala Glu Lys Glu Arg
188               515                      520                      525
189   Arg Lys Ser Gly Leu Ser Ser Arg Val Gln Phe Arg Asn Gln Gly Ser
190   530                      535                      540
191   Glu Pro Lys Tyr Thr Gln Glu Leu Thr Leu Lys Arg Gln Lys Gln Lys
192   545                      550                      555                      560
193   Val Cys Met Glu Glu Thr Leu Trp Leu Gln Asp Asn Ile Arg Asp Lys

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194				565				570				575	
195	Leu	Arg	Pro	Ile	Pro	Ile	Thr	Ala	Ser	Val	Glu	Ile	Gln
196				580				585				590	
197	Ser	Arg	Arg	Arg	Val	Asn	Ser	Leu	Pro	Glu	Val	Leu	Pro
198				595				600				605	
199	Ser	Asp	Glu	Pro	Lys	Thr	Ala	His	Ile	Asp	Val	His	Phe
200				610				615				620	
201	Gly	Cys	Gly	Asp	Asp	Asn	Val	Cys	Asn	Ser	Asn	Leu	Lys
202				625				630				635	
203	Lys	Phe	Cys	Thr	Arg	Glu	Gly	Asn	Gln	Asp	Lys	Phe	Ser
204								645				650	
205	Ile	Gln	Lys	Gly	Val	Pro	Glu	Leu	Val	Leu	Lys	Asp	Gln
206				660				665				670	
207	Ala	Leu	Glu	Ile	Thr	Val	Thr	Asn	Ser	Pro	Ser	Asn	Pro
208				675				680				685	
209	Thr	Lys	Asp	Gly	Asp	Asp	Ala	His	Glu	Ala	Lys	Leu	Ile
210				690				695				700	
211	Pro	Asp	Thr	Leu	Thr	Tyr	Ser	Ala	Tyr	Arg	Glu	Leu	Arg
212				705				710				715	
213	Glu	Lys	Gln	Leu	Ser	Cys	Val	Ala	Asn	Gln	Asn	Gly	Ser
214								725				730	
215	Cys	Glu	Leu	Gly	Asn	Pro	Phe	Lys	Arg	Asn	Ser	Asn	Val
216				740				745				750	
217	Leu	Val	Leu	Ser	Thr	Thr	Glu	Val	Thr	Phe	Asp	Thr	Pro
218				755				760				765	
219	Ile	Asn	Leu	Lys	Leu	Glu	Thr	Thr	Ser	Asn	Gln	Asp	Asn
220				770				775				780	
221	Ile	Thr	Ala	Lys	Ala	Lys	Val	Val	Ile	Glu	Leu	Leu	Ser
222				785				790				795	
223	Gly	Val	Ala	Lys	Pro	Ser	Gln	Val	Tyr	Phe	Gly	Gly	Thr
224								805				810	
225	Glu	Gln	Ala	Met	Lys	Ser	Glu	Asp	Glu	Val	Gly	Ser	Leu
226				820				825				830	
227	Glu	Phe	Arg	Val	Ile	Asn	Leu	Gly	Lys	Pro	Leu	Thr	Asn
228				835				840				845	
229	Ala	Thr	Leu	Asn	Ile	Gln	Trp	Pro	Lys	Glu	Ile	Ser	Asn
230				850				855				860	
231	Leu	Leu	Tyr	Leu	Val	Lys	Val	Glu	Ser	Lys	Gly	Leu	Glu
232				865				870				875	
233	Cys	Glu	Pro	Gln	Lys	Glu	Ile	Asn	Ser	Leu	Asn	Leu	Thr
234								885				890	
235	Asn	Ser	Arg	Lys	Lys	Arg	Glu	Ile	Thr	Glu	Lys	Gln	Ile
236				900				905				910	
237	Arg	Lys	Phe	Ser	Leu	Phe	Ala	Glu	Arg	Lys	Tyr	Gln	Thr
238				915				920				925	
239	Ser	Val	Asn	Val	Asn	Cys	Val	Asn	Ile	Arg	Cys	Pro	Leu
240				930				935				940	
241	Asp	Ser	Lys	Ala	Ser	Leu	Ile	Leu	Arg	Ser	Arg	Leu	Trp
242				945				950				955	
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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/088,639A

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